

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/430,035

AU 1812

DATE: 03/28/96

TIME: 11:48:15

INPUT SET: S9572.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANT: Eaton, Dan L.  
de Sauvage, Frederic J.

(ii) TITLE OF INVENTION: MPL LIGAND

(iii) NUMBER OF SEQUENCES: 21

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.  
(B) STREET: 460 Point San Bruno Blvd  
(C) CITY: South San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94080

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WinPatin (Genentech)

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/430035  
(B) FILING DATE: 27-Apr-1995  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/196689  
(B) FILING DATE: 15-FEB-1994

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/185607  
(B) FILING DATE: 21-JAN-1994

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/176553  
(B) FILING DATE: 03-JAN-1994

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Winter, Daryl B.  
(B) REGISTRATION NUMBER: 32,637  
(C) REFERENCE/DOCKET NUMBER: P0871P2D2

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/430,035DATE: 03/28/96  
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47  
48 (ix) TELECOMMUNICATION INFORMATION:  
49 (A) TELEPHONE: 415/225-1249  
50 (B) TELEFAX: 415/952-9881  
51 (C) TELEX: 910/371-7168  
52  
53 (2) INFORMATION FOR SEQ ID NO:1:  
54  
55 (i) SEQUENCE CHARACTERISTICS:  
56 (A) LENGTH: 42 amino acids  
57 (B) TYPE: Amino Acid  
58 (D) TOPOLOGY: Linear  
59  
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
61  
62 Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu  
63 -16 -15 -10 -5  
64  
65 Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys  
66 1 5 10  
67  
68 Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu  
69 15 20 25 26  
70  
71 (2) INFORMATION FOR SEQ ID NO:2:  
72  
73 (i) SEQUENCE CHARACTERISTICS:  
74 (A) LENGTH: 390 base pairs  
75 (B) TYPE: Nucleic Acid  
76 (C) STRANDEDNESS: Single  
77 (D) TOPOLOGY: Linear  
78  
79 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
80  
81  
82 GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT 50  
83  
84 CACCTCTCCT CATCTAAGAA TTG CTC CTC GTG GTC ATG CTT 91  
85 Leu Leu Leu Val Val Met Leu  
86 -16 -15 -10  
87  
88 CTC CTA ACT GCA AGG CTA ACG CTG TCC AGC CCG GCT CCT 130  
89 Leu Leu Thr Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro  
90 -5 1  
91  
92 CCT GCT TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT 169  
93 Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg  
94 5 10 15  
95  
96 GAC TCC CAT GTC CTT CAC AGC AGA CTG GTGA GAAC TCCCAA 210  
97 Asp Ser His Val Leu His Ser Arg Leu  
98 20 25 26  
99

RAW SEQUENCE LISTING  
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100 CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA CTCCCAGGAA 260  
101  
102 GACACCATCA CTTCCTCTAA CTCCTTGACC CAATGACTAT TCTTCCCATA 310  
103  
104 TTGTCCCCAC CTACTGATCA CACTCTCTGA CAAGAATTAT TCTTCACAAT 360  
105  
106 ACAGCCCGCA TTTAAAAGCT CTCGTCTAGA 390  
107

108 (2) INFORMATION FOR SEQ ID NO:3:  
109

110 (i) SEQUENCE CHARACTERISTICS:  
111 (A) LENGTH: 390 base pairs  
112 (B) TYPE: Nucleic Acid  
113 (C) STRANDEDNESS: Single  
114 (D) TOPOLOGY: Linear  
115

116 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
117

118  
119 TCTAGACGAG AGCTTTTAAA TGCGGGCTGT ATTGTGAAGA ATAATTCTTG 50  
120  
121 TCAGAGAGTG TGATCAGTAG GTGGGGACAA TATGGGAAGA ATAGTCATTG 100  
122  
123 GGTCAAGGAG TTAGAGGAAG TGATGGTGTC TTCCTGGGAG TATGGGTGTC 150  
124  
125 TTACCAGTTA CGCGGATAAA GGGGATAATG TTGGGAGTTC TCACCAGTCT 200  
126  
127 GCTGTGAAGG ACATGGGAGT CACGAAGCAG TTTACTGAGG ACTCGGAGGT 250  
128  
129 CACAAGCAGG AGGAGCCGGG CTGGACAGCG TTAGCCTTGC AGTTAGGAGA 300  
130  
131 AGCATGACCA CGAGGAGCAA TTCTTAGATG AGGAGAGGTG AGGTTGAAAG 350  
132  
133 ATGAGGAGGA AATCATTGTC AGCTGGTATT CCAGGAATTC 390  
134

135 (2) INFORMATION FOR SEQ ID NO:4:  
136

137 (i) SEQUENCE CHARACTERISTICS:  
138 (A) LENGTH: 353 amino acids  
139 (B) TYPE: Amino Acid  
140 (D) TOPOLOGY: Linear  
141

142 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
143

144 Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr  
145 -21 -20 -15 -10  
146  
147 Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu  
148 -5 1 5  
149  
150 Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser  
151 10 15 20  
152

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/430,035

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153	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val
154	25					30					35				
155															
156	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln
157	40					45					50				
158															
159	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu
160	55					60					65				
161															
162	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr
163	70					75					80				
164															
165	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu
166	85					90					95				
167															
168	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro
169	100					105					110				
170															
171	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu
172	115					120					125				
173															
174	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu
175	130					135					140				
176															
177	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Arg	Ala	Pro	Pro	Thr	Thr
178	145					150					155				
179															
180	Ala	Val	Pro	Ser	Arg	Thr	Ser	Leu	Val	Leu	Thr	Leu	Asn	Glu	Leu
181	160					165					170				
182															
183	Pro	Asn	Arg	Thr	Ser	Gly	Leu	Leu	Glu	Thr	Asn	Phe	Thr	Ala	Ser
184	175					180					185				
185															
186	Ala	Arg	Thr	Thr	Gly	Ser	Gly	Leu	Leu	Lys	Trp	Gln	Gln	Gly	Phe
187	190					195					200				
188															
189	Arg	Ala	Lys	Ile	Pro	Gly	Leu	Leu	Asn	Gln	Thr	Ser	Arg	Ser	Leu
190	205					210					215				
191															
192	Asp	Gln	Ile	Pro	Gly	Tyr	Leu	Asn	Arg	Ile	His	Glu	Leu	Leu	Asn
193	220					225					230				
194															
195	Gly	Thr	Arg	Gly	Leu	Phe	Pro	Gly	Pro	Ser	Arg	Arg	Thr	Leu	Gly
196	235					240					245				
197															
198	Ala	Pro	Asp	Ile	Ser	Ser	Gly	Thr	Ser	Asp	Thr	Gly	Ser	Leu	Pro
199	250					255					260				
200															
201	Pro	Asn	Leu	Gln	Pro	Gly	Tyr	Ser	Pro	Ser	Pro	Thr	His	Pro	Pro
202	265					270					275				
203															
204	Thr	Gly	Gln	Tyr	Thr	Leu	Phe	Pro	Leu	Pro	Pro	Thr	Leu	Pro	Thr
205	280					285					290				

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206
207 Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro
208 295 300 305
209
210 Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His
211 310 315 320
212
213 Ser Gln Asn Leu Ser Gln Glu Gly
214 325 330 332
215
216 (2) INFORMATION FOR SEQ ID NO:5:
217
218 (i) SEQUENCE CHARACTERISTICS:
219 (A) LENGTH: 1798 base pairs
220 (B) TYPE: Nucleic Acid
221 (C) STRANDEDNESS: Single
222 (D) TOPOLOGY: Linear
223
224 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
225
226
227 GCGTCTTCCT ACCCATCTGC TCCCCAGAGG GCTGCCTGCT GTGCACTTGG 50
228
229 GTCCTGGAGC CCTTCTCCAC CCGGATAGAT TCCTCACCCT TGGCCCGCCT 100
230
231 TTGCCCCACC CTACTCTGCC CAGAAGTGCA AGAGCCTAAG CCGCCTCCAT 150
232
233 GGCCCCAGGA AGGATTCAGG GGAGAGGCC CAAACAGGGA GCCACGCCAG 200
234
235 CCAGACACCC CGGCCAGA ATG GAG CTG ACT GAA TTG CTC CTC 242
236 Met Glu Leu Thr Glu Leu Leu Leu
237 -21 -20 -15
238
239 GTG GTC ATG CTT CTC CTA ACT GCA AGG CTA ACG CTG TCC 281
240 Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu Ser
241 -10 -5
242
243 AGC CCG GCT CCT CCT GCT TGT GAC CTC CGA GTC CTC AGT 320
244 Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser
245 1 5 10
246
247 AAA CTG CTT CGT GAC TCC CAT GTC CTT CAC AGC AGA CTG 359
248 Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
249 15 20 25
250
251 AGC CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA CCT GTC 398
252 Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
253 30 35
254
255 CTG CTG CCT GCT GTG GAC TTT AGC TTG GGA GAA TGG AAA 437
256 Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys
257 40 45 50
258

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